



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 190621

TO: Sean McGarry
Location: REM-2C18
Art Unit: 1635
Thursday, May 2006
Case Serial Number: 10/714796

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner McGarry,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

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190621

STIC-Biotech/ChemLib

From: McGarry, Sean
Sent: Friday, May 19, 2006 1:06 PM
To: STIC-Biotech/ChemLib
Subject: SEQ SEARCH 10/714,796

Sean McGarry 73484
AU 1635
571.272.0761
REM 2C18 Mailbox
PHP
10/714,796

Please, a length limited search of SEQ ID NO: 122 (nt \leq 75).

Thank You.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.

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Wed May 24 10:03:07 2006

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 10:56:45 ; Search time 2444 Seconds
(without alignments)
523.301 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgtggaattaccagccca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2571824

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:*
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15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	50	2	AR682287 Sequence
2	14.2	71.0	68	2	AR356566 Sequence
3	14.2	71.0	68	2	AR538122 Sequence
4	13.6	68.0	29	2	AR044889 Sequence
5	13.6	68.0	29	2	AR096454 Sequence
6	13.6	68.0	29	2	174371 Sequence 34
7	13.6	68.0	45	2	155019 Sequence 43
8	13.6	68.0	50	2	AX960383 Sequence
9	13.6	68.0	51	2	CQ007345 Sequence
10	13.2	66.0	22	2	BD177702 Process f
11	13.2	66.0	22	2	CQ830789 Sequence
12	13.2	66.0	22	2	AX503513 Sequence
13	13.2	66.0	41	2	AX574446 Sequence
14	13.2	66.0	44	2	BD177703 Process f
15	13.2	66.0	44	2	CQ830790 Sequence
16	13.2	66.0	44	2	AX503514 Sequence
17	13.2	66.0	65	2	AX484110 Sequence
18	13	65.0	60	2	BD006973 Artificialia

19	12.8	64.0	20	2	AR241114 Sequence
20	12.8	64.0	21	2	AR072146 Sequence
21	12.8	64.0	24	2	AR429847 Sequence
22	12.8	64.0	24	2	AX042025 Sequence
23	12.8	64.0	56	2	CS191956 Sequence
24	12.8	64.0	59	2	BD006952 Artificialia
25	12.8	64.0	65	2	CQ559344 Sequence
26	12.8	64.0	69	11	AY538960 Champodo
27	12.6	63.0	20	2	BD016897 Rice-orig
28	12.6	63.0	20	2	DD176246 Verificat
29	12.6	63.0	20	2	AX803985 Sequence
30	12.6	63.0	24	2	CS027277 Sequence
31	12.6	63.0	24	2	CS027278 Sequence
32	12.6	63.0	31	2	BD016889 Rice-orig
33	12.6	63.0	42	2	AR071190 Sequence
34	12.6	63.0	51	5	AY082067 Homo Bapi
35	12.6	63.0	59	2	CS052969 Sequence
36	12.6	63.0	59	2	CS183920 Sequence
37	12.6	63.0	59	2	AX600107 Sequence
38	12.6	63.0	60	2	CQ541589 Sequence
39	12.6	63.0	65	2	CQ560799 Sequence
40	12.6	63.0	65	2	AX483910 Sequence
41	12.4	62.0	17	2	AX532402 Sequence
42	12.4	62.0	17	2	AX532403 Sequence
43	12.4	62.0	17	2	AX532404 Sequence
44	12.4	62.0	17	2	AX532405 Sequence
45	12.4	62.0	25	2	AX534464 Sequence

ALIGNMENTS

RESULT 1	AR682287	Sequence 1716 from patent US 6905827.	50 bp	DNA	linear	PAT 12-SBP-2005
LOCUS	AR682287	Sequence 1716 from patent US 6905827.	50 bp	DNA	linear	PAT 12-SBP-2005
DEFINITION	AR682287	Sequence 1716 from patent US 6905827.	50 bp	DNA	linear	PAT 12-SBP-2005
ACCESSION	AR682287	Sequence 1716 from patent US 6905827.	50 bp	DNA	linear	PAT 12-SBP-2005
VERSION	AR682287.1	GI:74464057	50 bp	DNA	linear	PAT 12-SBP-2005
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 50)					
AUTHORS	Mohlgenuth,J., Fry,K., Woodward,R. and Ly,N.					
TITLE	Methods and compositions for diagnosing or monitoring auto immune and chronic inflammatory diseases					
JOURNAL	Patent: US 6905827-A 1716 14-JUN-2005;					
FEATURES	Expression Diagnostics, Inc.; So. San Francisco, CA					
source	Location/Qualifiers					
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	/organism="unknown"					
	/mol_type="genomic DNA"					
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Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;					
Qy	1 ACGTGAATTATACAGCC 19					
Db	19 ACGTGAATTATACAGAC 37					
RESULT 2	AR356566	Sequence 2684 from patent US 6593114.	68 bp	DNA	linear	PAT 17-AUG-2003
LOCUS	AR356566	Sequence 2684 from patent US 6593114.	68 bp	DNA	linear	PAT 17-AUG-2003
DEFINITION	AR356566	Sequence 2684 from patent US 6593114.	68 bp	DNA	linear	PAT 17-AUG-2003
ACCESSION	AR356566	Sequence 2684 from patent US 6593114.	68 bp	DNA	linear	PAT 17-AUG-2003
VERSION	AR356566.1	GI:33762650	68 bp	DNA	linear	PAT 17-AUG-2003
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
	Unclassified.					

REFERENCE 1 (bases 1 to 68)
AUTHORS Kunach,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and

TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 2684 15-JUL-2003;
Human Genome Sciences, Inc.; Rockville, MD

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Best Local Similarity 84.2%; Pred. No. 7.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTGAATTATACGACCA 20
DB 35 CATGAATTATCCGCGCA 53

RESULT 3
LOCUS AR538122 68 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2684 from patent US 6737248.
ACCESSION AR538122
VERSION AR538122.1 GI:53929339
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 68)

AUTHORS Kunach,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6737248-A 2684 18-MAY-2004;
Human Genome Sciences, Inc.; Rockville, MD

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Best Local Similarity 84.2%; Pred. No. 7.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTGAATTATACGACCA 20
DB 35 CATGAATTATCCGCGCA 53

RESULT 4
LOCUS AR044889 29 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 43 from patent US 5817759.
ACCESSION AR044889
VERSION AR044889.1 GI:5966354
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 29)

AUTHORS Margolskee,R.F.
TITLE Gustducin polypeptides and fragments
JOURNAL Patent: US 5817759-A 43 06-OCT-1998;
Location/Qualifiers
FEATURES
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGACCA 20
DB 9 ACGTTTATTTATTCAGCCA 28

RESULT 5
LOCUS AR096454 29 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 43 from patent US 6008000.
ACCESSION AR096454
VERSION AR096454.1 GI:10025269
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 29)

AUTHORS Margolskee,R.F.
TITLE Gustducin materials and methods
JOURNAL Patent: US 6008000-A 43 28-DEC-1999;
Location/Qualifiers
FEATURES
source 1..29
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/mol_type="unassigned DNA"

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Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGACCA 20
DB 9 ACGTTTATTTATTCAGCCA 28

RESULT 6
LOCUS I74371 29 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 34 from patent US 5688662.
ACCESSION I74371
VERSION I74371.1 GI:3010512
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 29)

AUTHORS Margolskee,R.F.
TITLE Gustducin polynucleotides, vectors, host cells and recombinant
JOURNAL Patent: US 5688662-A 34 18-NOV-1997;
Location/Qualifiers
FEATURES
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/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGACCA 20
DB 9 ACGTTTATTTATTCAGCCA 28

RESULT 7
LOCUS I55019 45 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 43 from patent US 5646156.
ACCESSION I55019
VERSION I55019.1 GI:2476222

ORIGIN

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclasseified.
AUTHORS 1 (bases 1 to 45)
TITLE Jacobson,M.A., Johnson,R.G. and Salvatore,C.A.
JOURNAL Inhibition of eosinophil activation through A3 adenosine receptor
FEATURES antagonism
Patent: US 5646156-A 43 08-JUL-1997;
source Location/Qualifiers
1..45
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Qy 1 ACGTGAATTATACCGCA 20
Db 32 ACCGAGATGACACCGCA 13
RESULT 8
LOCUS AX960383 50 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 59 from Patent WO03102192.
ACCESSION AX960383
VERSION AX960383.1 GI:40880510
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Oligo used for the 2D6 assembly"
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ACGTGAATTATACCGCA 20
Db 16 ACGGAGACTTACCGCA 35
RESULT 9
LOCUS CQ007345 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 5985 from Patent WO0147944.
ACCESSION CQ007345
VERSION CQ007345.1 GI:41013986
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof
JOURNAL Patent: WO 0147944-A 5985 05-JUL-2001;
Curegen Corporation (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Accession number cg43960450"
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Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ACGTGAATTATACCGCA 20
Db 13 ACGTCAATTATACCGCA 32
RESULT 10
BD177702/c 22 bp DNA linear PAT 16-APR-2003
LOCUS BD177702/c
DEFINITION Process for producing L-glutamine by fermentation and L-glutamine-producing microorganism.
ACCESSION BD177702
VERSION BD177702.1 GI:30014964
KEYWORDS JP 2002300887-A/14.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Unknown
OS JP 2002300887-A/14
PN 15-OCT-2002
PD 30-MAY-2001 JP 2001162806
PI JUN NAKAMURA, KAYO MORIGUCHI, HIROSHI IZUI, NOBUKI KAWASHIMA, PI
PC TSIYOSHI NAKAMATSU OSAMU KURAHASHI
PC C12N1/21, C12N1/13, C12N9/12, C12P13/14, C12N1/21, C12R1/15, PC
(C12N1/21, C12R1/15), (C12N9/12, C12R1/15), (C12P13/14, C12R1/13), PC
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FH Key
FH Location/Qualifiers
FT source 1..22
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1..22
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Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ACGTGAATTATACCGC 18
Db 19 ACGTCAATTATACCGC 2
RESULT 11
LOCUS CQ830789/c 22 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 16 from Patent EP1424398.
ACCESSION CQ830789

VERSION C0830789.1 GI:50251068
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura,J., Izui,H., Moriyuchi,K., Kawashima,H., Nakamatsu,T. and Kurahashi,O.
TITLE Method for producing L-glutamine by fermentation and L-glutamine producing bacterium
JOURNAL Patent: EP 1424398-A 16 02-JUN-2004;
Ajinomoto Co., Inc. (JP)
FEATURES location/Qualifiers
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/note="Description of Artificial Sequence: primer"
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Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACGTGAATTATACGAGC 18
19 ACGTTCATTATACGAGC 2
DB 19 ACGTTCATTATACGAGC 2
RESULT 12
AX503513/C 22 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 16 from Patent EP1229121.
DEFINITION AX503513
ACCESSION AX503513
VERSION AX503513.1 GI:23385805
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura,J., Izui,H., Moriyuchi,K., Kawashima,H., Nakamatsu,T. and Kurahashi,O.
TITLE Method for producing L-glutamine by fermentation and L-glutamine producing bacterium
JOURNAL Patent: EP 1229121-A 16 07-AUG-2002;
Ajinomoto Co., Inc. (JP)
FEATURES location/Qualifiers
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/db_xref="taxon:32630"
/note="primer"
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QY 1 ACGTGAATTATACGAGC 18
19 ACGTTCATTATACGAGC 2
DB 19 ACGTTCATTATACGAGC 2
RESULT 13
AX574446 41 bp DNA linear PAT 07-JAN-2003
LOCUS Sequence 18 from Patent WO02068629.
DEFINITION AX574446
ACCESSION AX574446
VERSION AX574446.1 GI:27551770
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
AUTHORS Pachuk,C.J. and McCallus,D.E.
TITLE Dna constructs for cytoplasmic and mitochondrial expression and methods of making and using same
JOURNAL Patent: WO 02068629-A 18 06-SEP-2002;
Wyeeth (US)
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/db_xref="taxon:9606"
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Best Local Similarity 83.3%; Pred. No. 2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GTGGAATTATACGAGCA 20
4 GCGGAATTGTACCGCCA 21
DB 4 GCGGAATTGTACCGCCA 21
RESULT 14
BD177703 44 bp DNA linear PAT 16-APR-2003
LOCUS BD177703/C
DEFINITION Process for producing L-glutamine by fermentation and L-glutamine-producing microorganism.
ACCESSION BD177703
BD177703.1 GI:30014965
VERSION BD177703
KEYWORDS JP 2002300887-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 44)
AUTHORS Nakamura,J., Moriyuchi,K., Izui,H., Kawashima,N., Nakamatsu,T. and Kurahashi,O.
TITLE Process for producing L-glutamine by fermentation and L-glutamine-producing microorganism
JOURNAL Patent: JP 2002300887-A 15 15-OCT-2002;
AJINOMOTO CO. INC
COMMENT OS Artificial Sequence
OS Unknown
PN JP 2002300887-A/15
PD 15-OCT-2002
PF 30-MAY-2001 JP 2001162806
PI JUN NAKAMURA,KAYO MORIYUCHI,HIROSHI IZUI,NOBUKI KAWASHIMA,PI TSUYOSHI NAKAMATSU,OSAMU KURAHASHI
PC C12N15/09,C12N1/21,C12P13/14/(C12N1/21,C12R1:15),PC (C12N1/21,C12R1:13), (C12N9/12,C12R1:15), (C12N9/12,C12R1:13), PC (C12P13/14,C12R1:15), (C12P13/14,C12R1:13), C12N15/00 CC
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/mol_type="genomic DNA"
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Best Local Similarity 83.3%; Pred. No. 2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACGTGAATTATACGAGC 18
41 ACGTTCATTATACGAGC 24
DB 41 ACGTTCATTATACGAGC 24
RESULT 15

CO830790/c CO830790 44 bp DNA linear PAT 12-JUL-2004
LOCUS Sequence 17 from Patent EPI424398.
DEFINITION CO830790
ACCESSION CO830790
VERSION CO830790.1 GI:50251069
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Nakamura,T., Izui,H., Moriguchi,K., Kawashima,H., Nakamatsu,T. and
Kurahashi,O.
TITLE Method for producing L-glutamine by fermentation and L-glutamine
JOURNAL producing bacterium
Patent: EP 1424398-A 17 02-JUN-2004;
Ajinomoto Co., Inc. (JP)
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Best Local Similarity 83.3%; Pred. No. 2e+05;
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Db 41 ACGTCAATTATACGAGC 24
Search completed: May 23, 2006, 11:42:24
Job time : 2446 secs

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OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 10:37:30 ; Search time 290 Seconds
(without alignments)
480.845 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20
Sequence: 1 acgtggaattacacagcca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5508782

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_8:*

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- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	13	ADR72358
2	15.2	76.0	40	10	ADD24544
3	14.8	74.0	32	3	ABK12019
4	14.2	71.0	50	6	ABZ01725
5	14.2	71.0	68	2	AAV76995
6	14.2	71.0	75	10	ACD93498
7	13.8	69.0	25	9	ACI58064
8	13.8	69.0	25	9	ACI58693
9	13.8	69.0	25	9	ACI58692
10	13.6	68.0	29	2	AAO51108
11	13.6	68.0	29	2	AAV54426
12	13.6	68.0	29	2	AAZ49047
13	13.6	68.0	29	8	ABT15720
14	13.6	68.0	29	9	ACA62089
15	13.6	68.0	30	12	ADP09053
16	13.6	68.0	30	14	ADY02430
17	13.6	68.0	45	2	AAT07608
18	13.6	68.0	45	2	AAT00676

19	13.6	68.0	50	12	ADJ87572	AdJ87572 Human cyt
20	13.6	68.0	51	4	AAJ32777	AAJ32777 Human SNP
21	13.2	66.0	22	6	ABO82104	ABO82104 Brevibact
22	13.2	66.0	22	12	AD080107	AD080107 Glutamate
23	13.2	66.0	26	2	AAT87460	AAT87460 Chicken/h
24	13.2	66.0	40	6	ABK96453	ABK96453 PCR prime
25	13.2	66.0	41	6	ADH13895	ADH13895 Human max
26	13.2	66.0	44	6	ABK96460	ABK96460 PCR prime
27	13.2	66.0	44	6	ABO82105	ABO82105 Brevibact
28	13.2	66.0	44	12	AD080108	AD080108 Glutamate
29	13.2	66.0	65	6	ABZ27463	ABZ27463 Candida e
30	13	65.0	60	2	AAV23214	AAV23214 Lactococc
31	13	65.0	60	15	AE886265	AE886265 MML3 prob
32	12.8	64.0	20	10	ABX78268	ABX78268 Human b1f
33	12.8	64.0	21	2	AAV76378	AAV76378 Zea mays
34	12.8	64.0	21	6	AAU42928	AAU42928 Maize bug
35	12.8	64.0	21	14	ABC74822	ABC74822 Maize ete
36	12.8	64.0	24	3	AAU66328	AAU66328 DSP5 spec
37	12.8	64.0	29	3	AAU04617	AAU04617 Polymorph
38	12.8	64.0	40	15	ABP10355	ABP10355 B19 virus
39	12.8	64.0	40	15	ABP10354	ABP10354 B19 virus
40	12.8	64.0	41	4	AAH75822	AAH75822 Human G p
41	12.8	64.0	56	14	ABD81864	ABD81864 Hyperimmu
42	12.8	64.0	59	2	AAV23193	AAV23193 Lactococc
43	12.8	64.0	60	6	ABK98622	ABK98622 Lambda CP
44	12.8	64.0	60	9	ACD13873	ACD13873 L. lactis
45	12.8	64.0	60	14	ADZ62209	ADZ62209 Murine ch

ALIGNMENTS

RESULT 1	
ADR72358	ADR72358 standard; DNA; 20 BP.
ID	ADR72358
XX	ADR72358;
AC	02-DEC-2004 (first entry)
XX	
DT	Antisense oligo targeted to human kinesin-like 1, ISIS 344894.
XX	
DE	Antisense; kinesin-like 1; N2 kinesin; b1mc kinesin; autoimmu disease;
XX	cellular proliferation; cancer; B-cell leukemia; systemic sclerosis;
KW	carpal tunnel syndrome; Raynaud's phenomenon; polyarteritis;
KW	Sjogren's syndrome; rheumatoid arthritis; polyarteritis;
KW	systemic lupus erythematosus; human; ss; ISIS 344894; rat.
XX	
OS	Homo sapiens.
OS	Rattus sp.
OS	Synthetic.
XX	
XX	
FT	Key
FT	modified_base
FT	1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphorochioate nucleotide. All cytosines
FT	are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are
FT	2'-methoxyethyl nucleotides."
PN	US2004180847-A1.
XX	
PD	16-SEP-2004.
XX	
PF	17-NOV-2003; 2003US-00714796.
XX	
PR	23-MAY-2002; 2002US-00156603.
XX	
PA	(DOB1/) DOBIE K W.
PA	(KOLL/) KOLLER E.
XX	
PI	Doble KW, Koller E;
XX	

DR WPI; 2004-652550/63.

XX New antisense compound 8 to 80 nucleobases in length targeted to a

PT nucleic acid molecule encoding kinesin-like 1, useful for treating an

PT animal having a disease or condition such as cancer, tumor, autoimmune

PT disease.

XX

XX Claim 35; SEQ ID NO 122; 110pp; English.

XX

XX The present invention relates to antisense compounds, compositions and

CC methods for modulating the expression of kinesin-like 1. The superfamily

CC of kinesins function as molecular engines to bind and transport vesicles

CC and organelles along microtubules using energy supplied by ATP. Kinesin-

CC like 1, a member of the N2 (also called bimc) family of kinesins, is

CC involved in separating the chromosomes by directing their movement along

CC microtubules in the bipolar spindle. Kinesin-like 1 is also known as

CC KNSL1, Eg5, Heeg5, HKSP, Kif11, thyroid interacting protein 5 and TKIP5.

CC Inhibition of kinesin-like 1 may be a target for arresting cellular

CC proliferation in cancer, due to its central role in mitosis. Expression

CC of kinesin-like 1 expression may contribute to other disease states such

CC as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome,

CC Raynaud's phenomenon, systemic sclerosis, Sjogren's syndrome, rheumatoid

CC arthritis, polymyositis and polyarteritis. Kinesin-like 1 is an

CC autoantigen identified in systemic lupus erythematosus. The invention

CC relates to antisense nucleic acid oligomers, targeted to the gene

CC encoding kinesin-like 1. Also provided are methods of screening for

CC modulators of kinesin-like 1 and to methods of modulating the expression

CC of kinesin-like 1. At least a portion of the compound hybridises with RNA

CC to form an oligonucleotide-RNA duplex. It has at least one modified

CC internucleoside linkage, sugar moiety, or nucleobase. It has at least one

CC 2'-O-methoxyethyl sugar moiety, phosphorothioate internucleoside linkage,

CC or one cytosine which is a 5-methylcytosine. The antisense compound may

CC comprise an antisense nucleic acid molecule that is specifically

CC hybridisable with a 5'-untranslated region (UTR), with a start region,

CC with a coding region, with a 3'-UTR, with an intron, or with an intron-

CC exon junction of a nucleic acid molecule encoding kinesin-like 1.

CC Oligonucleotides were synthesised via solid phase P(III) phosphoramidite

CC chemistry. The present sequence is an antisense oligo targeted to human

CC kinesin-like 1, ISIS #344894.

XX

XX Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

XX

XX Query Match 100.0%; Score 20; DB 13; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.1;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGACCA 20

DB 1 ACGTGAATTATATACGACCA 20

XX

XX RESULT 2

XX ADD24544/c

XX ID ADD24544 standard; DNA; 40 BP.

XX

XX ADD24544;

XX

XX 15-JAN-2004 (first entry)

XX

XX DNA polymerase III subunit protein related PCR primer, SEQ ID NO 63.

XX

XX DNA polymerase III replicase; dnaB; hola; holB; holC; holD; holE; dnaX;

XX dnaN; SSB; dnaQ; bacterial DNA replication; bacterial infection;

XX PCR; primer; ss.

XX

XX Unidentified.

XX

XX WO200292769-A2.

XX

XX 21-NOV-2002.

XX

XX 14-MAY-2002; 2002WO-US015111.

XX

PR 14-MAY-2001; 2001US-0290725P.

PR 05-NOV-2001; 2001US-0332644P.

XX

XX (REPL-) REPLICDYNE INC.

XX

XX Bullard JM, Janjic N, Mchenry CS;

XX

XX WPI; 2003-120672/11.

XX

XX Screening for a compound that modulates the activity of *Y. pestis* and/or

PT *P. aeruginosa* DNA polymerase III replicase, useful for reducing bacterial

PT DNA replication and infection in animals, plants, humans and surrounding

PT environment.

XX

XX Example 38; SEQ ID NO 63; 388pp; English.

XX

XX The invention relates to a novel screening method for a compound that

CC modulates the activity of a DNA polymerase III replicase. The novel

CC method comprises contacting an isolated replicase with at least one test

CC compound under conditions permissive for replicase activity, and

CC comparing the activity of the replicase in the presence and absence of

CC the test compound, where a change in the activity of the replicase

CC indicates a compound that modulates the activity of the replicase. The

CC replicase comprises an isolated nucleic acid from *Yersinia pestis* or a

CC *Pseudomonas aeruginosa* encoding a DNA polymerase III subunit protein. The

CC DNA polymerase III subunit proteins include dnaB, hola, holB, holC, holD,

CC hola, dnaX, dnaN, SSB, dnaQ, and dnaQ. The methods and compositions of

CC the present invention are useful for reconstituting replicases and

CC polymerases for sequencing, amplification and screening for compounds

CC which modulate the function of the polymerase or replicase particularly

CC in bacterial DNA replication, thereby reducing bacterial infection in

CC animals, plants, humans and the surrounding environment. This

CC polynucleotide sequence represents a PCR primer relating to the DNA

CC polymerase III subunit proteins of the invention.

XX

XX Sequence 40 BP; 8 A; 9 C; 9 G; 14 T; 0 U; 0 Other;

XX

XX Query Match 76.0%; Score 15.2; DB 10; Length 40;

XX Best Local Similarity 85.0%; Pred. No. 7.3e+02;

XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGACCA 20

DB 27 ACGTGAATTACGACGACCA 8

XX

XX RESULT 3

XX ABK12019

XX ID ABK12019 standard; DNA; 32 BP.

XX

XX ABK12019;

XX

XX 05-JUN-2002 (first entry)

XX

XX Human cyclin B2 related B1 anti-sense RT-PCR primer.

XX

XX RT-PCR; primer; reverse transcriptase; ss; B1.

XX

XX Homo sapiens.

XX

XX KR99081550-A.

XX

XX 15-NOV-1999.

XX

XX 30-APR-1998; 98KR-00015566.

XX

XX 30-APR-1998; 98KR-00015566.

XX

XX 30-APR-1998; 98KR-00015566.

XX

XX (KIMD/) KIM D G.

XX

XX Kim DG, Yoo GR, Shin HS;

XX

XX WPI; 2000-617338/59.

XX

Best Local Similarity 84.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTGAATTATACGACCA 20
| | | | | | | | | | | | | | | | | | | | | |
DB 35 CATGGAATTATCCCGCCA 53

RESULT 6
ACD93498

ID ACD93498 standard; cDNA; 75 BP.

AC ACD93498;

DT 23-SEP-2003 (first entry)

DE Human colon cancer cell expressed cDNA #1910.

XX Open reading frame detection; genome sequencing; colon cancer;
KM breast cancer; population genome analysis; genetic shift; cancer;
KM antibiotic resistance; antibiotic non-tolerance; congenital disease;
KM agriculture; food crop genome; resistance gene; retrovirus;
KM influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KM gene; ss.

OS Homo sapiens.

PN US2002155438-A1.

PD 24-OCT-2002.

PF 27-SEP-1999; 99US-00406117.

PR 20-NOV-1998; 98US-00196716.

PA (SIMP/) SIMPSON A J G.

PA (NETO/) NETO E D.

PA (BREN/) BRENTANI R R.

PI Simpson AJG, Neto ED, Brentani RR;

XX WPI; 2003-182626/18.

PT Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.

PS Example 9; Page 297; 959pp; English.

XX The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. Further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a fetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,

CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library

XX SQ Sequence 75 BP; 14 A; 30 C; 9 G; 22 T; 0 U; 0 Other;

Query Match Score 14.2; DB 10; Length 75;

Best Local Similarity 84.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGACC 19
| | | | | | | | | | | | | | | | | | | | | |
DB 50 ACGTGAATTCTACCATCC 68

RESULT 7
ACIS8064/C

ID ACIS8064 standard; DNA; 25 BP.

AC ACIS8064;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 58055.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;
KM cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFPY-) APFYMATRIX INC.

PI Miltmann MP;

XX WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 58055; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labeled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-

blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 4 A; 4 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TGGAAATTATACCAAGCA 20
|||||
DB 25 TGGAAATTATACCAAGCA 9

RESULT 8

ACIS8693/c
ID ACIS8693 standard; DNA; 25 BP.

ACIS8693;

13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 58684.

EST; seq; probe; expressed sequence tag; microarray; gene expression;
genetic variation; biallelic marker; polymorphism; human;
cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFY-) AFFYMETRIX INC.

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 58684; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of mRNA molecules by

primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 5 A; 4 C; 5 G; 11 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TGGAAATTATACCAAGCA 20
|||||
DB 24 TGGAAATTATACCAAGCA 8

RESULT 9

ACIS8692/c
ID ACIS8692 standard; DNA; 25 BP.

ACIS8692;

13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 58683.

EST; seq; probe; expressed sequence tag; microarray; gene expression;
genetic variation; biallelic marker; polymorphism; human;
cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFY-) AFFYMETRIX INC.

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 58683; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been

CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

SO Sequence 25 BP; 4 A; 4 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;
 Best Local Similarity 88.2%; Pred. No. 3.8e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TGGAAATTATACCAAGCA 20
 |||||
 DB 24 TCGAATTATACCAAGCA 8

RESULT 10

AAO51108
 ID AAO51108 standard; DNA; 29 BP.

AC AAO51108;

DT 25-MAR-2003 (revised)
 DT 24-MAY-1994 (first entry)

DE Alpha subunit specific PCR primer for rat gustducin cDNA.

KM Taste modifying agent; ligand; antiligand; binding activity; taste;
 KM taste receptor cells; sweet; bitter; sweet; salty; sour; ss;
 KM amplification.

OS Synthetic.

PN WO9321337-A1.

PD 28-OCT-1993.

PF 08-APR-1993; 93WO-US003279.

PR 09-APR-1992; 92US-00868353.

PA (MARG/) MARGOLSKEE R F.

PI Margolskee RF;

DR WPI: 1993-351746/44.

DR P-PSDB; AAR42435.

PT New gustducin alpha subunit protein - used for identifying taste
 PT modifying agents which mimic or inhibit sweet, bitter, salty or sour
 PT tastes.

PS Disclosure; Page 12; 50pp; English.

CC Six degenerate oligonucleotide primer sets were made to correspond to
 CC regions of amino acids highly conserved among previously described G
 CC protein alpha subunits. The primers were used for PCR with DNA from a
 CC taste cell library as template. Partial clones and further PCR primers
 CC (shown) were used to isolate a composite gustatory alpha subunit clone or
 CC gustducin gene clone. See also AAO51098-107. (Updated on 25-MAR-2003 to
 CC correct PN field.)

SO Sequence 29 BP; 8 A; 7 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 2; Length 29;
 Best Local Similarity 80.0%; Pred. No. 4.9e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ACGTGAATTATACCAAGCA 20
 |||||
 DB 9 ACGTTAATTATTTTCAGCA 28

RESULT 11

AAV54426
 ID AAV54426 standard; cDNA; 29 BP.

AC AAV54426;

DT 21-DEC-1998 (first entry)

DE Nucleotide sequence of PCR primer 10.

KM PCR; primer; amplification; rat; gustducin alpha-subunit; taste;
 KM inhibition; ss.

OS Synthetic.

OS Rattus sp.

PN US5817759-A.

PD 06-OCT-1998.

PF 20-MAR-1995; 95US-00407804.

PR 09-APR-1992; 92US-00868353.

PR 08-APR-1993; 93US-00045801.

PA (LING-) LINGUAGEN CORP.

PI Margolskee RF;

DR WPI: 1998-556463/47.

PT New purified and isolated rat gustducin alpha-subunit polypeptide - can
 PT be delivered to taste receptor cells to modify taste, e.g. mimic or
 PT inhibit sweet and/or bitter tastes.

PS Example 1; Col 39-40; 25pp; English.

CC This is the nucleotide sequence of a PCR primer (derived from the
 CC conserved regions of rat gustducin) used for amplification in the method
 CC of the invention where the rat gustducin alpha-subunit protein used in
 CC the method of the invention to modify taste. The peptides or fragments
 CC can be delivered to taste receptor cells to modify taste, e.g. mimic or
 CC inhibit sweet and/or bitter tastes. The polypeptides can also be used in
 CC screening assays for taste-modifying agents

SO Sequence 29 BP; 8 A; 7 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 2; Length 29;
 Best Local Similarity 80.0%; Pred. No. 4.9e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ACGTGAATTATACCAAGCA 20
 |||||
 DB 9 ACGTTAATTATTTTCAGCA 28

RESULT 12
 AAZ49047
 ID AAZ49047 standard; DNA; 29 BP.

AC AAZ49047;

DT 31-MAR-2000 (first entry)

DE PCR primer for taste cell specific G protein.

KM PCR primer; taste cell specific G protein; taste modifying agent;
 KM gustducin; transducin; taste inhibitor; ss.

OS Rattus sp.

PN US6008000-A.

PD 28-DEC-1999.
XX
PF 28-JUL-1998; 98US-00124807.
XX
PR 09-APR-1992; 92US-00868353.
PR 20-MAR-1995; 95US-00407804.
XX
PA (LING-) LINGUAGEN CORP.
XX
PI Margolskee RF;
XX
DR WPI; 2000-096373/08.
XX
PT Identifying taste modifying agents which can interact with taste
XX receptors to mimic or block natural taste stimulants.
PS
SQ Example 1; Col 7; 25pp; English.
XX
CC This sequence represents a PCR primer used to isolate a rat taste cell
CC specific G protein. The invention relates to a method of identifying a
CC taste modifying agent, comprising: (a) incubating phospholipid vesicles
CC having gustducin alpha-subunit or transducin alpha-subunit and G protein
CC beta- and gamma-subunits associated in biologically active form with the
CC agent and GTPgammaS; and (b) determining the rate of GTPgammaS binding by
CC the alpha-subunit in comparison to a standard rate where an increase in
CC the rate of binding indicates that the agent is a taste stimulator and a
CC inhibitor. The method is useful for identifying taste modifying agents
CC which can interact with taste receptors to mimic, block or inhibit
CC particular tastes
XX
SQ Sequence 29 BP; 8 A; 7 C; 5 G; 9 T; 0 U; 0 Other;
XX
Query Match 68.0%; Score 13.6; DB 3; Length 29;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 ACGTGAATTATACGACCA 20
DB 9 ACGTTAATTATTTCAGCA 28
XX
RESULT 13
ABT15720
ID ABT15720 standard; DNA; 29 BP.
XX
AC ABT15720;
XX
DT 28-MAR-2003 (first entry)
XX
DE Human cancer/cectis antigen PCR primer - SEQ ID No 11.
XX
KW Human; PCR; primer; gene therapy; vaccine; cancer; cancer/cectis antigen;
KW CT antigen; ss.
XX
OS Homo sapiens.
XX
PN WO200278526-A2.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009808.
XX
PR 30-MAR-2001; 2001US-0280718P.
PR 20-APR-2001; 2001US-0285154P.
PR 05-OCT-2001; 2001US-0327432P.
PR 22-JAN-2002; 2002US-00054683.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX (CORR) CORNELL RES FOUND INC.
XX Old LJ, Scanlan MJ, Chen Y;
XX

DR WPI; 2003-040608/03.
XX
XX Diagnosing cancer comprises contacting a biological sample isolated from
PT a subject with an agent that specifically binds to a nucleic acid
PT molecule, its expression product or fragment or an antibody that binds to
PT the product or fragment.
XX
PS Example 2; Page 68; 155pp; English.
XX
CC The invention comprises a method for diagnosing cancer, the method
CC involves detecting the DNA or protein sequences of human cancer/cectis
CC (CT) antigens that are disclosed in the invention. The method of the
CC invention is useful for detecting/diagnosing, treating and monitoring a
CC cancer or condition characterised by the expression of a human CT
CC antigen. The present DNA sequence represents a PCR primer used in an
CC example of the invention
XX
SQ Sequence 29 BP; 7 A; 13 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 68.0%; Score 13.6; DB 8; Length 29;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 ACGTGAATTATACGACCA 20
DB 3 ACGTGAATTATACGACCA 22
XX
RESULT 14
ACA62089
ID ACA62089 standard; DNA; 29 BP.
XX
AC ACA62089;
XX
DT 19-AUG-2003 (first entry)
XX
DE G protein alpha subunit PCR primer #10.
XX
KW Taste; taste modification; gustducin alpha subunit;
KW ligand binding activity; antilgand binding activity;
KW G protein alpha subunit; conserved region; PCR; primer; ss.
XX
OS Synthetic.
XX
PN US200303119-A1.
XX
PD 16-JAN-2003.
XX
PF 21-FEB-2001; 2001US-00789996.
XX
PR 09-APR-1992; 92US-00868353.
PR 08-APR-1993; 93US-00045801.
PR 20-MAR-1995; 95US-00407804.
PR 28-JUL-1998; 98US-00124807.
PR 20-OCT-1999; 99US-00421796.
XX
PA (LING-) LINGUAGEN CORP.
XX
PI Margolskee RF;
XX
DR WPI; 2003-466043/44.
XX
XX Novel gustducin alpha-subunit polypeptide possessing ligand/antilgand
PT binding activity or immunological property specific to gustducin, for
PT identifying peptide ligand/antilgand of gustducin and taste modifying
PT agent.
XX
PS Example 1; Page 4; 27pp; English.
XX
CC The invention describes a purified and isolated gustducin alpha subunit
CC polypeptide (1), fragment or variant possessing at least one
CC ligand/antilgand binding activity or immunological property specific to
CC gustducin. (1) is useful for identifying a peptide ligand/antilgand of

CC gustducin, by contacting (1) with peptides and isolating peptides which
CC bind to (1), and for identifying taste modifying agent. An antibody is
CC useful for modifying taste which involves delivering Ab to taste receptor
CC cell. The antibody is useful for purifying (1) and for blocking or
CC inhibiting ligand/antiligand binding activities of gustducin. This
CC sequence represents a primer designed using a G protein conserved region
CC and used to create a primer for the construction of a G protein cDNA
CC library for isolation of gustducin
XX
XX Sequence 29 BP; 8 A; 7 C; 5 G; 9 T; 0 U; 0 Other;

Query Match	68.0%;	Score 13.6;	DB 9;	Length 29;
Best Local Similarity	80.0%;	Pred No. 4.9e+03;		
Matches 16;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

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QY      1 ACGTGAATTATACCAGCCA 20
          ||| ||||| |||||
Db      9 ACGTTAATTATTTCAGCCA 28

```

RESULT 15

ID ADP09053 standard; DNA; 30 BP.

ADP09053;

DT 26-AUG-2004 (first entry)

DE PCR primer 54 used to genotype human chromogranin B polymorphism.

KW breast cancer; cytostatic; gene therapy; human; chromogranin B; CHGB; survival; prognosis

KW single nucleotide polymorphism.

OS Homo sapiens.

PN WO2004047767-A2.

PD 10-JUN-2004.

PF 25-NOV-2003; 2003WO-US037966.

PR 25-NOV-2002; 2002US-0429136P.

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PT or absence of one or more nucleotide polymorphic variations, useful for identifying mutations and/or tracking breast cancer

XX	Environ	2000	26(5):545-551
XX	Environ	2000	26(5):545-551

The invention relates to a novel method for identifying a subject at risk of breast cancer which comprises detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject. The method of the invention has cytostatic applications and may be useful for identifying a risk of breast cancer, as well as therapeutic and prophylactic treatments that specifically target breast cancer, such as gene therapy. The current sequence is that of a PCR primer of the invention which was used to genotype single nucleotide polymorphisms within human chromosome 18 (CHGB;pericentromeric 1pSG1) DNA which is located at chromosomal position 20pter-p12.

Sequence 30 BP; 8 A; 8 C; 7 G; 7 T; 0 U; 0 Other;

Query Match	Score	DB	Length
68.0%;	13.6;	12;	30;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATACCAGCCA 20
||| | | | | | | | |
Db 1 ACGTTGATGAGACCAGCCA 20

Search completed: May 23, 2006, 11:01:29
Job time : 293 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 11:01:41 ; Search time 4305 Seconds
(without alignments)
259.788 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgfgaattatcacgcca 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 495048

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc3:*
3: gb_esc4:*
4: gb_esc5:*
5: gb_esc6:*
6: gb_esc7:*
7: gb_esc8:*
8: gb_esc9:*
9: gb_esc10:*
10: gb_esc11:*
11: gb_esc12:*
12: gb_esc13:*
13: gb_esc14:*
14: gb_esc15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.8	84.0	69	14	BX230540 Danio rerio
2	14.2	71.0	75	1	AI903657 OY-PR032-
3	13.8	69.0	69	4	CB552792 MMSPO038
4	13.6	68.0	70	14	AL771470 Arabidops
5	13.6	68.0	70	4	CD001979 C4B12 sub
6	13.2	66.0	63	13	CM131880 104_515_1
7	13.2	66.0	66	10	N71991 YZ96D01.B1
8	13.2	66.0	69	13	DU440790 1098402106
9	13.2	66.0	69	11	AP149581 AP149581
10	13.2	66.0	75	12	CC155989 XST053 Ba
11	12.8	64.0	63	1	AL732271 AL732271
12	12.8	64.0	71	8	CV303709 t963602.b
13	12.8	64.0	75	3	BU634669 016C12 in
14	12.6	63.0	45	11	AZ480835 1M0302109
15	12.6	63.0	56	6	AK219728 Mus muscu
16	12.6	63.0	60	13	CL308290 03F0096-0
17	12.6	63.0	65	10	DV237624 A2FLD67TO
18	12.6	63.0	67	11	AZ645226 1M0510U03
19	12.6	63.0	69	10	DY249203 CSTFBID07

20	12.6	63.0	72	12	CG466064 01S0542-0
21	12.6	63.0	72	14	AL757528 Arabidops
22	12.6	63.0	73	14	BX691027 Arabidops
23	12.4	62.0	54	5	CD530824 08C01 Ara
24	12.4	62.0	55	1	AJ235741 Arabidops
25	12.4	62.0	55	11	AZ658522 1M0535A18
26	12.4	62.0	59	13	CM391650 F5BD001F0
27	12.4	62.0	60	8	CN931823 000428AF8
28	12.4	62.0	72	14	BX290465 Arabidops
29	12.2	61.0	49	1	AI424311 t590D05.X
30	12.2	61.0	55	1	AM085274 Arabidops
31	12.2	61.0	57	11	BH847350 SALK_0528
32	12.2	61.0	57	14	CR360294 Arabidops
33	12.2	61.0	62	14	AJ595367 Arabidops
34	12.2	61.0	62	14	CR009942 Reverse s
35	12.2	61.0	63	5	CD948686 SNG_22 Ge
36	12.2	61.0	63	11	BH790863 SALK_0580
37	12.2	61.0	64	13	CL210752 F023F03 G
38	12.2	61.0	67	14	AJ622651 Drosophila
39	12.2	61.0	67	14	CR397249 Arabidops
40	12.2	61.0	69	1	AA449410 zxc04f12.r
41	12.2	61.0	69	3	BP075817 BP075817
42	12.2	61.0	69	11	AZ826432 2M0102112
43	12.2	61.0	70	2	BF779346 3179-63 h
44	12.2	61.0	71	8	C0745478 TGESTZPD0
45	12.2	61.0	72	11	BZ354686 SALK_1256

ALIGNMENTS

RESULT 1
LOCUS BX230540 69 bp DNA linear GSS 29-JAN-2003
DEFINITION Danio rerio genomic clone DKEX-253D18, genomic survey sequence.
ACCESSION BX230540
VERSION BX230540.1 GI:28064690
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 69)
Humphray, S.J., Huckle, E. and Durham, J.L.
AUTHORS Direct Submission
TITLE Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
JOURNAL Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humphrey@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 253D18, 253D18
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
KEYWORDS Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
source location/Qualifiers
1..69
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-253D18"
/issue_type="Testis"
/note="vector pIndigoBAC-536"

ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 69;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACGGAAATTATACAGCA 20
|||
DB 50 ACATGCAATTATACAGCA 69
|||

RESULT 2

AI903657 75 bp mRNA linear EST 30-MAR-2000
LOCUS AI903657
DEFINITION QV-BT032-190299-122 BT032 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI903657
VERSION AI903657.1 GI:6494044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 75)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,
Nagel, M.A., da Silva, W. Jr., Zagdo, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?ti=QVat2-QV-BT032-122.html
kt3=190299&ct=1)
Seq primer: puc 18 forward.
Location/Qualifiers
FEATURES
source
1..75
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"
/clone_lib="BT032"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI. A mini-library was made by cloning products derived
from ORBSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

Query Match 71.0%; Score 14.2; DB 1; Length 75;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACGTGAATTATACGACC 19
Db 50 ACCTGGAATCTACCATCC 68

RESULT 3
CB552792/c 69 bp mRNA linear EST 01-JUN-2003
LOCUS CB552792
DEFINITION MMSF0038_E07 MMSF Macaca mulatta cDNA, mRNA sequence.
ACCESSION CB552792
VERSION CB552792.1 GI:31301987
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 69)
AUTHORS Katze, M.G., Bumgarner, R., Korch, M., Feldman, R., Amjadi, M. and
Holzman, T.
TITLE Expressed sequence tags from Rhesus macaque spleen
JOURNAL Unpublished (2002)
COMMENT Contact: Holzman T
Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6035
Email: ted@locke.hs.washington.edu
Similar to GenBank entry HSM804066 AL832755 Homo sapiens mRNA; cDNA
DKFZp686A0927 (from clone DKFZp686A0927). 7/2002
Plate: MMSF0038 row: E column: 07.
FEATURES
source
1..69
/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
/sex="male"
/cell_type="monocytes"
/dev_stage="adult"
/clone_lib="MMSF"
/note="Organ: spleen"
Location/Qualifiers

Query Match 69.0%; Score 13.8; DB 4; Length 69;
Best Local Similarity 88.2%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 TGAATTATACGACCA 20
Db 40 TGAAGTACTACGCA 24

RESULT 4
AL771470 69 bp DNA linear GSS 01-APR-2004
LOCUS AL771470
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-180E10-013611,
genomic survey sequence.
ACCESSION AL771470
VERSION AL771470.1 GI:21533672
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weishaar, B.
TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 69)
AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Welschaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany.

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F1B16. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source Location/Qualifiers

1.69
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_id="GK-180B10-013611"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (71) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ51514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 68.0%; Score 13.6; DB 14; Length 69;
Best Local Similarity 80.0%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATTCAGCCA 20
Db 17 ACGAGAAATTGACCGCTA 36

RESULT 5 CD001979 70 bp mRNA linear EST 01-MAY-2003
LOCUS C4B12 subtracted cochlea cDNA library Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION CD001979
VERSION CD001979.1 GI:30307306
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 70)
Luijendijk,M.W.J., van de Pol,T.J.R., van Duinhoven,G., den Hollander,A.I., ten Caat,J., van Limpe,V., Brunner,H.G., Kremer,H. and Cremers,F.P.M.
Cloning, characterization and mRNA expression of novel human fetal cochlea cDNAs
Unpublished (2003)
Contact: Kremer H
Department of Human Genetics
University Medical Center Nijmegen
P.O. Box 9101, 6500 HB Nijmegen, The Netherlands
Tel: +31 24 3614017
Fax: +31 24 3540488
Email: h.kremer@umcn.nl
The insert was not completely sequenced
Insert Length: 70 Std Error: 0.00
Seq primer: T7 GTAAATGCACTCACTATAGCGGG
POLYA=No.

FEATURES
source Location/Qualifiers

1.70
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="cochlea"

/dev_stage="16-22 week fetus"
/lab_host="TOP10F"
/clone_id="Sorghum bicolor cochlea cDNA library"
/clone_lib="Sorghum bicolor cochlea cDNA library"
/note="Organ: ear; Vector: PCR1; Subtraction of cochlea cDNA (tester) was performed with the PCR-select cDNA Subtraction Kit (Clontech). Driver cDNA consisted of a mixture of cDNAs from brain, kidney, liver, heart, skeletal muscle, placenta, stomach (mucosal layer) and psoas muscle. Tester and driver cDNAs were digested by BsaI; adaptors were ligated to the tester. Two rounds of subtractive hybridization were performed, followed by two suppression PCR reactions. Subtracted PCR products were ligated into a T/A vector (Invitrogen)."

ORIGIN

Query Match 68.0%; Score 13.6; DB 4; Length 70;
Best Local Similarity 80.0%; Pred. No. 3.5e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATTCAGCCA 20
Db 3 ACTTGAAATATTCAGCCA 22

RESULT 6 CW131880 63 bp DNA linear GSS 29-OCT-2004
LOCUS CW131880/c
DEFINITION 104_515_11115912_116_34797_096 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 1115912, genomic survey sequence.
ACCESSION CW131880
VERSION CW131880.1 GI:54824427
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 63)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,D., Bradford,K., McMenamy,D., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korff,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
Plos Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 515 row: a column: 24
Seq primer: T3 Reverse
Class: methylation filtered
High quality sequence stop: 63.

FEATURES
source Location/Qualifiers

1.63
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="RTx623"
/db_xref="taxon:4558"
/clone_id="11115912"
/clone_lib="Sorghum methylation filtered library (LibID: 104)"
/note="Organ: leaf; Vector: pBCKS(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCKS(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

	Query Match	66.0%	Score 13.2;	DB 13;	Length 63;
	Best Local Similarity	83.3%;	Pred. No. 5.6e+04;		
	Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
Oy	3 GTGGAAATTATACCAAGCCA 20 N71991				
RESULT 7	N71991	66 bp mRNA linear EST 15-MAR-1996			
LOCUS	y296b01.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290857.3, similar to gb:U1968.nal MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);, mRNA sequence.				
ACCESSION	N71991				
VERSION	N71991.1 GI:1228703				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 66) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,U., Rifkin,D., Rohlfing,T., Soares,M., Tan,F., Trivaskis,E., Waterson,R., Williamson,A., Wohldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995)				
TITLE	The WashU-Merck EST Project				
JOURNAL	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 850L, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810				
COMMENT	Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality Seq primer: m13 -40 forward High quality sequence stop: 1. Location/Qualifiers: 1..66 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:3883987" /db_xref="taxon:9606" /clone="IMAGE:290857" /sex="Male" /tissue_type="melanocyte" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares melanocyte 2NBHM" /note="Vector: pUT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' TGTTACAATCTGAAGTCGACGCCGCACATTTTTTTTTTTTTTTT 3'] double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT3 vector (Pharmacia). Library constructed by Bento Soares and M.Felina Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."				
FEATURES					
source					
ORIGIN					
Query Match	66.0%; Score 13.2; DB 10; Length 66;				
Best Local Similarity	78.9%; Pred. No. 5.6e+04;				
Matches 15; Conservative	0; Mismatches 4; Indels 0; Gaps 0;				
OY	1 ACGTGAATTATACCAACC 19 N71991				
DB	42 AGGTGAGAGTNTCCAGCC 60				

```

RESULT 8
DU440790 66 bp DNA linear GSS 06-OCT-2005
LOCUS 1098421061035 CHORI-243 Ovis aries genomic clone CH243-244P19,
DEFINITION
ACCESSION
DU440790
VERSION
DU440790.1 GI:77194680
KEYWORDS
GSS.
ORGANISM
Ovis aries (sheep)
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
1 (bases 1 to 66)
Kirkness, E., Shetty, J., de Jong, P., McEwan, J. C., Oddy, H. and
Cockett, N.
Ovine BAC End Sequences from Library CHORI-243
Unpublished (2004)
Other GSSs: 1098415783056
Contact: Ewen Kirkness
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
Email: ekirknes@tigr.org
Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVJTC; http://www.venterlinstitute.org/).
Original Trace: 1098421061035 Trace TI: gnl|txl|918984698
Insert Length: 184000 Std Error: 0.00 row: P column: 19
Seq primer: T7
Class: BAC ends.
FEATURES
Source
Location/Qualifiers
1..66
/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-244P19"
/sex="Male"
/cell_type="Blood"
/clone_id="CHORI-243"
/notes="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"
ORIGIN
Query Match 66.0%; Score 13.2; DB 13; Length 66;
Best Local Similarity 83.3%; Pred. No. 5.66+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Ov 3 GTGGAATTATACGACCA 20
|||
29 GTGGACTTTTACGACGA 46
|||
RESULT 9
AF149581/c 69 bp DNA linear GSS 12-JUN-20000
LOCUS AF149581 Human chromosome 18q21 from exon-trapping Homo sapiens
DEFINITION
ACCESSION AF149581
VERSION AF149581.1 GI:8485912
KEYWORDS
GSS.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 69)
Chen, H., Huo, Y., Patel, S., Zhu, X., Swift-Scanlan, T., Reeves, R. H.,
DePaulo, R. Jr., Rose, C. A. and McIntosh, M. G.

```


1. TITLE	Gene identification using exon amplification on human chromosome 18q21: implications for bipolar disorder									
2. JOURNAL	Mol. Psychiatry 5 (5), 502-509 (2000)									
3. COMMENT	Contact: Chen H Psychiatry and Behavioral Sciences Johns Hopkins University School of Medicine 600 N. Wolfe Street, Baltimore, MD 21287, USA Email: hewei@chlink.welch.jhu.edu Class: exon-trapped.									
4. FEATURES	Location/Qualifiers 1..69 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /map="18q21" /clone="3a19" /clone_lib="Human chromosome 18q21 from exon-trapping"									
5. ORIGIN										
6. Query Match	66.0%	Score 13.2;	DB 11;	Length 69;						
7. Best Local Similarity	83.3%	Pred. No. 5.6e+04;								
8. Matches	15;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;	
9. Cy	1	ACGTGCAATTATACGACC	18							
10. Db	45	AGGTGCAATTATTCATC	28							
11. RESULT 10										
12. LOCUS	CC155989	75 bp	mRNA	linear	GSS 25-APR-2003					
13. DEFINITION	XST053 BayGenomics Gene Trap Library pGT2Tnpfs Mus musculus cDNA, mRNA sequence.									
14. ACCESSION	CC155989									
15. VERSION	CC155989.1	GI:30109345								
16. KEYWORDS	GSS.									
17. SOURCE	Mus musculus (house mouse)									
18. ORGANISM	Mus musculus									
19. COMMENT	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.									
20. REFERENCE	1 (bases 1 to 75)									
21. AUTHORS	BayGenomics.									
22. TITLE	http://baygenomics.ucsf.edu/									
23. JOURNAL	unpublished (2001)									
24. COMMENT	Contact: BayGenomics Bay Area Functional Genomics Consortium (BayGenomics) Email: info@baygenomics.ucsf.edu Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. Es cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=XST053									
25. FEATURES	Class: Gene Trap.									
26. SOURCE	Location/Qualifiers 1..75 /organism="Mus musculus" /mol_type="mRNA" /strain="129 Ola" /db_xref="taxon:10090" /sex="Male" /cell_type="Embryonic stem cell" /clone_lib="BayGenomics Gene Trap Library pGT2Tnpfs" /note="Vector: pGT2Tnpfs"									
27. ORIGIN										
28. Query Match	66.0%	Score 13.2;	DB 12;	Length 75;						
29. Best Local Similarity	83.3%	Pred. No. 5.7e+04;								
30. Matches	15;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;	
31. Cy	2	CGTGAATTATACGACC	19							

DB	46 CCGTGAAGTTTACCGGCC 63			
RESULT 11				
LOCUS	AL732271	63 bp	mRNA	linear EST 07-MAY-2002
DEFINITION	AL732271 pool_AK_11b_v_SPE Homo sapiens cDNA, mRNA sequence.			
ACCESSION	AL732271			
VERSION	AL732271.1	GI:20501682		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominidae; Homo.			
	1 (bases 1 to 63)			
	Ascroft,K., Bethel,G., Bye,J.M., Howell,G.R., Huckie,E.J. and			
	Sheridan,E.			
TITLE	Homo sapiens EST sequence			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: The Sanger Centre The Sanger Centre Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK Email: humquerry@sanger.ac.uk Sanger Centre name : scdd10643.158623Sa Homo sapiens EST sequence. This sequence was generated as part of the Wellcome Trust Sanger Institute's program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool AK_11b v SPE cDNA library. Further information can be found at http://www.sanger.ac.uk/Teams/Team69/ .			
FEATURES	Location/Qualifiers			
SOURCE	1..63			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/map="20"			
	/clone_11b="pool_AK_11b_v_SPE"			
ORIGIN				
Query Match	64.0%;	Score 12.8;	DB 1;	Length 63;
Best Local Similarity	87.5%;	Pred. No. 9.1e+04;		
Matches 14;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
OY	1 ACGTGGAATTATACCA 16			
DB	34 ACGTGGAATTCACCA 49			
RESULT 12				
LOCUS	CV303709	71 bp	mRNA	linear EST 23-SEP-2004
DEFINITION	tg63e02.b7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA			
ACCESSION	sequence.-			
CV303709				
VERSION	CV303709.1	GI:52621042		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			
	Sciuognathi; Muroidae; Muridae; Murinae; Mus.			
	1 (bases 1 to 71)			
	Dike,S., Ballia,V.S., Nascimento,L.U., Xuan,Z., Ou,J., Zutavern,T.,			
	Palmer,L.E., Hannon,G., Zhang,M.Q. and McCombie,W.R.			
TITLE	The mouse genome: Experimental examination of gene predictions and			
JOURNAL	transcriptional start sites			
PUBMED	Genome Res. 14 (12), 2424-2429 (2004)			
CONTACT:	Balijsa VS			

McCombie Laboratory
Cold Spring Harbor Laboratory
500 Sunnyside Blvd, Woodbury, NY 11797, USA
Fax: 516 422 4109
Email: balija@csnl.org.

FEATURES

source

1. 71
Location/Qualifiers

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_1lb="Mouse 5', RACE clones"
/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments amplified from 5' RACE cDNA generated from 15 pooled mouse tissues and stages: 7, 11, 15, & 17-day total embryo, whole brain, eye, kidney, liver, lung, prostate, submaxillary gland, smooth muscle, spleen, testes and uterus."

ORIGIN

Query Match 64.0%; Score 12.8; DB 8; Length 71;
Best Local Similarity 87.5%; Pred. No. 9.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 TGAATTATACCAGCC 19
13 TGGCATGTGACCAGCC 28

RESULT 13
BU634669 75 bp mRNA linear EST 23-SEP-2002
LOCUS 016C12 Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
DEFINITION sequence.

ACCESSION BU634669
VERSION BU634669.1 GI:23301924
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 75)
Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S.
and Wellinder,K.G.

TITLE EST sequencing of Erysiphe cichoracearum infected Arabidopsis plants

JOURNAL Unpublished (2002)
COMMENT Institute: Karen G. Wellinder
Institute for Biotechnology
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.au.dk.

FEATURES

source

1. 75
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/dev_stage="Plant 3 weeks old, three days post infection"
/clone_1lb="Infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT selected."

ORIGIN

Query Match 64.0%; Score 12.8; DB 3; Length 75;
Best Local Similarity 87.5%; Pred. No. 9.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 TGAATTATACCAGCC 19
6 TGGAGTATACCAGCC 21

RESULT 14
A2480835 45 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0302109R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0302109 R, genomic survey sequence.

ACCESSION A2480835
VERSION A2480835.1 GI:10641900
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Isiam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedernausern,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: 1 column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers

FEATURES

source

1. 45
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0302109"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (91|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 63.0%; Score 12.6; DB 11; Length 45;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 CGTGAATTATACCAAGCA 20
 |||||
 21 CGGGGATCTTACCAAGCA 39

RESULT 15

AK219728 56 bp mRNA linear HTC 23-NOV-2004
 LOCUS AK219728/c

DEFINITION Mus musculus cDNA, clone: Y2G0149G13, strand: minus, reference: ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000069765, based on BLAT search.

ACCESSION

AK219728

VERSION AK219728.1 GI:56043905

KEYWORDS

HTC; ASSETS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1

Marahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S., Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M., Hayashizaki, Y. and Carninci, P.

Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas

Nat. Methods 1, 233-239 (2004)

JOURNAL

2 (bases 1 to 56)

REFERENCE

Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N., Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M., Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watanahiki, A. and Hayashizaki, Y.

Direct Submission
 Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA libraries, hybridizing of

single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures

(alternative spliced exon), ligating of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pFLCI vector. (Reference).

Location/Qualifiers

1..56

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="Y2G0149G13"

/cell_line="mixture of B16-F10Y and melan-c"

/cell_type="mixture of melanoma cell and melanocyte cell"

/clone_lib="Alternative Splicing Library L3"

/note="strand:minus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000069765, based on BLAT search"

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ENST:ENSMUST0000069765, based on BLAT search"

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ENST:ENSMUST0000069765, based on BLAT search"

ENST:ENSMUST0000069765, based on BLAT search"

ORIGIN

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 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ACGTGAATTATACCAAGCC 19
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29 AAGTGAAGTATACCAAGCC 11
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Search completed: May 23, 2006, 12:54:23
 Job time : 4309 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 11:29:33 ; Search time 68 Seconds
(without alignments)
550.326 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgtgactatcacagca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 1518026

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents NA:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCtUS COMB.seq:*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	50	US-10-131-827-1716	Sequence 1716, Ap
2	14.2	71.0	50	US-10-131-831-1716	Sequence 1716, Ap
3	14.2	71.0	68	US-08-956-171E-2684	Sequence 2684, Ap
4	14.2	71.0	68	US-08-781-986A-2684	Sequence 2684, Ap
5	13.8	69.0	25	US-09-396-196G-39721	Sequence 39721, A
6	13.6	68.0	29	US-07-868-353A-34	Sequence 34, Appl
7	13.6	68.0	29	US-08-407-804-43	Sequence 43, Appl
8	13.6	68.0	29	US-09-124-807-43	Sequence 43, Appl
9	13.6	68.0	45	US-08-233-009-43	Sequence 43, Appl
10	13.4	67.0	25	US-09-396-196G-80092	Sequence 80092, A
11	13.4	67.0	25	US-09-396-196G-80093	Sequence 80093, A
12	13.4	67.0	25	US-09-396-196G-116886	Sequence 116886, A
13	12.8	64.0	20	US-09-844-552A-85	Sequence 85, Appl
14	12.8	64.0	21	US-08-410-784A-7	Sequence 7, Appl
15	12.8	64.0	21	US-10-179-562-41	Sequence 41, Appl
16	12.8	64.0	24	US-09-564-357-13	Sequence 13, Appl
17	12.8	64.0	29	US-09-304-233-817	Sequence 817, App
18	12.6	63.0	27	US-07-945-156A-4	Sequence 4, Appl
19	12.6	63.0	42	US-08-610-728B-8	Sequence 8, Appl
20	12.4	62.0	25	US-09-396-196G-123214	Sequence 123214, A
21	12.2	61.0	22	US-08-253-030-26	Sequence 26, Appl
22	12.2	61.0	24	US-09-947-770-32	Sequence 32, Appl
23	12.2	61.0	25	US-09-217-101-5	Sequence 5, Appl

24	12.2	61.0	25	US-09-577-005-62	Sequence 62, Appl
25	12.2	61.0	30	US-08-513-968-69	Sequence 69, Appl
26	12.2	61.0	30	US-09-576-160B-20	Sequence 20, Appl
27	12.2	61.0	30	US-09-576-160B-24	Sequence 24, Appl
28	12.2	61.0	40	US-08-399-696-31	Sequence 31, Appl
29	12.2	61.0	73	US-08-282-030-18	Sequence 18, Appl
30	12.2	61.0	73	PCR-US95-10219-18	Sequence 18, Appl
31	12	60.0	30	US-09-038-227-45	Sequence 45, Appl
32	12	60.0	50	US-08-171-388-478	Sequence 478, App
33	12	60.0	50	US-08-123-936-478	Sequence 478, App
34	12	60.0	50	US-08-475-228A-478	Sequence 478, App
35	12	60.0	50	US-08-482-080A-478	Sequence 478, App
36	12	60.0	50	US-09-354-947-478	Sequence 478, App
37	12	60.0	50	US-09-993-346-478	Sequence 478, App
38	12	60.0	50	US-10-131-827-982	Sequence 982, App
39	12	60.0	50	US-10-131-831-982	Sequence 982, App
40	12	60.0	50	PCR-US93-12388-478	Sequence 478, App
41	12	60.0	71	US-08-255-236-18	Sequence 18, App
42	12	60.0	71	US-09-123-728-34	Sequence 34, Appl
43	11.8	59.0	20	US-09-198-452A-6355	Sequence 6355, Ap
44	11.8	59.0	25	US-09-396-196G-113221	Sequence 113221, A
45	11.8	59.0	26	PCR-US92-06821A-25	Sequence 25, Appl

ALIGNMENTS

```
RESULT 1
US-10-131-827-1716
; Sequence 1716, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131, 827
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1716
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1716
Query Match          71.0% Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 ACGTGACTTATACAGCC 19
DB      19 ACGTGAATTATACAGAC 37
RESULT 2
US-10-131-831-1716
; Sequence 1716, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
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FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: Patentin version 3.1
SEQ ID NO: 1716
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-831-1716

Query Match      71.0%; Score 14.2; DB 5; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  ACGTGAATTATACGACC 19
Db      19  ACGTGAATTATATCAGAC 37

RESULT 3
US-08-956-171E-2684
Sequence 2684, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gail H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2684:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2684:
US-08-956-171E-2684

Query Match      71.0%; Score 14.2; DB 3; Length 68;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  CGTGAATTATACCGCCA 20
Db      35  CATGAATTATCCCGCCA 53

RESULT 4
US-08-781-986A-2684
Sequence 2684, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2684:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-2684

Query Match      71.0%; Score 14.2; DB 3; Length 68;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  CGTGAATTATACCGCCA 20
Db      35  CATGAATTATCCCGCCA 53

RESULT 5
US-09-396-196G-39721
Sequence 39721, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
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;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FASTSeq for Windows Version 4.0
;; SEQ ID NO 39721
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-396-196G-39721

Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGGATTATTCAGCCA 20
DB 1 TGAATTATTCAGCCA 17

RESULT 6

US-07-868-353A-34
; Sequence 34, Application US/07868353A
; Patent No. 5688662
; GENERAL INFORMATION:
; APPLICANT: Margolskee, Robert F.
; TITLE OF INVENTION: Guaducun Materials and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; TELEFAX: (312) 984-9740
; TELEPHONE: (312) 346-5750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-868-353A-34

Query Match 68.0%; Score 13.6; DB 2; Length 29;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAATTATTCAGCCA 20
DB 9 ACGTTTAATTATTCAGCCA 28

RESULT 7

US-08-407-804-43
; Sequence 43, Application US/08407804
; Patent No. 5817759
; GENERAL INFORMATION:
; APPLICANT: Margolskee, Robert F.
; TITLE OF INVENTION: Guaducun Materials and Methods
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,804
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/045,801
FILING DATE:
APPLICATION NUMBER: US 07/868/353

ATTORNEY/AGENT INFORMATION:
FILING DATE: 09-APR-1992
NAME: No. 5817759and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:

INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-407-804-43

Query Match 68.0%; Score 13.6; DB 2; Length 29;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAATTATTCAGCCA 20
DB 9 ACGTTTAATTATTCAGCCA 28

RESULT 8

US-09-124-807-43
; Sequence 43, Application US/09124807
; Patent No. 6008000
; GENERAL INFORMATION:
; APPLICANT: Margolskee, Robert F.
; TITLE OF INVENTION: Guaducun Materials and Methods
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124.807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/407,804
FILING DATE:
APPLICATION NUMBER: US 07/868/353
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6008000and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-124-807-43

Query Match 68.0%; Score 13.6; DB 3; Length 29;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAAATTATACGACCA 20
Db 9 ACGTTAATTATTACGCA 28

RESULT 9
US-08-233-009-43/c
Sequence 43, Application US/08233009
Patent No. 5646156
GENERAL INFORMATION:
APPLICANT: Jacobson, Marlene A
APPLICANT: Johnson, Robert G
APPLICANT: Salvatore, Christopher A
TITLE OF INVENTION: INHIBITION OF EOSINOPHIL
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O.Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,009
FILING DATE: 25-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19219
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3901
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-233-009-43

Query Match 68.0%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAAATTATACGACCA 20
Db 32 ACCGGAATGACACCGCA 13

RESULT 10
US-09-396-196G-80092/c
Sequence 80092, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80092
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-80092

Query Match 67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTGGAATTATACCG 17
Db 18 GTGGAAGTATACCG 4

RESULT 11
US-09-396-196G-80093/c
Sequence 80093, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80093
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-80093

Query Match 67.0%; Score 13.4; DB 3; Length 25;
-Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTGAATTATACCAG 17
|||
Db 15 GTGAAGATATACCAG 1

RESULT 12

US-09-396-196G-116886/C
; Sequence 116886, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116886
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-116886

Query Match 67.0%; Score 13.4; DB 3; Length 25;
-Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGAATTATACCAG 18
|||
Db 25 TGAATTATACCAG 11

RESULT 13

US-09-844-525A-85
; Sequence 85, Application US/09844525A
; Patent No. 6468796
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BIFUNCTIONAL APOPTOSIS REGULATOR EXPRESSION
; FILE REFERENCE: RTS-0230
; CURRENT APPLICATION NUMBER: US/09/844,525A
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 85
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-844-525A-85

Query Match 64.0%; Score 12.8; DB 3; Length 20;
-Best Local Similarity 87.5%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTGAATTATACCAG 18
|||
Db 1 GTGAATTATACCAG 16

RESULT 14
US-08-410-784A-7

; Sequence 7, Application US/08410784A

; Patent No. 5912413
; GENERAL INFORMATION:
; APPLICANT: MYERS, ALAN M.
; APPLICANT: JAMES, MARTHA G.
; TITLE OF INVENTION: ISOLATION OF SU1, A STARCH DEBRANCHING
; TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE
; TITLE OF INVENTION: SUGARY 1
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin and Hayes LLP
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,784A
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Ph.D., Holliday C
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: ISU-002XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-2290
; TELEFAX: 617-451-0313
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-410-784A-7

Query Match 64.0%; Score 12.8; DB 2; Length 21;
-Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAATTATACCAGCA 20
|||
Db 1 GGAATATACCAGCA 16

RESULT 15

US-10-179-562-41
; Sequence 41, Application US/10179562
; Patent No. 6995300
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; APPLICANT: James, Martha G.
; TITLE OF INVENTION: ISOLATION OF SU1, A STARCH DEBRANCHING
; TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE SUGARY 1
; FILE REFERENCE: ISU-002BX
; CURRENT APPLICATION NUMBER: US/10/179,562
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/256,741
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Zea mays
us-10-179-562-41

Query Match 64.0%; Score 12.8; DB 4; Length 21;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAATTATACGAGCCA 20
||| |||||
Db 1 GGGATCATACGAGCCA 16

Search completed: May 23, 2006, 11:37:08
Job time : 69 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 11:36:27 ; Search time 978 Seconds
(without alignments)
251.281 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgtggaattaccagcca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24330200

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-10-714-796-122
2	15.2	76.0	40	9	US-10-476-597-63
3	14.8	74.0	25	8	US-10-719-956-197295
4	14.8	74.0	25	9	US-10-719-900-135431
5	14.8	74.0	25	9	US-10-719-900-265411
6	14.8	74.0	50	16	US-11-175-859-7489
7	14.8	74.0	50	16	US-11-175-859-91821
8	14.4	72.0	25	9	US-10-719-900-962131
9	14.2	71.0	25	8	US-10-719-956-169821
10	14.2	71.0	25	8	US-10-719-956-169822
11	14.2	71.0	25	9	US-10-719-900-467341
12	14.2	71.0	25	10	US-10-956-157-15043
13	14.2	71.0	25	10	US-10-956-157-15044
14	14.2	71.0	25	10	US-10-956-157-190558
15	14.2	71.0	25	11	US-10-932-162A-135456
16	14.2	71.0	25	11	US-10-934-048A-79340
17	14.2	71.0	25	11	US-10-934-048A-78871

18	14.2	71.0	25	13	US-11-036-317-429637	Sequence 429637,
19	14.2	71.0	50	7	US-10-131-827-1716	Sequence 1716, Ap
20	14.2	71.0	68	2	US-08-781-986A-2684	Sequence 2684, Ap
21	14.2	71.0	68	8	US-10-329-624-2684	Sequence 2684, Ap
22	14.2	71.0	19	14	US-11-083-784-274670	Sequence 274670,
23	14.2	71.0	19	14	US-11-083-784-401583	Sequence 401583,
24	14.2	71.0	19	14	US-11-083-784-401591	Sequence 401591,
25	14.2	71.0	19	15	US-11-101-244-274670	Sequence 274670,
26	14.2	71.0	19	15	US-11-101-244-401583	Sequence 401583,
27	14.2	71.0	19	15	US-11-101-244-401591	Sequence 401591,
28	14.2	71.0	25	10	US-10-843-527-45153	Sequence 45153, A
29	14.2	71.0	25	10	US-10-843-527-193024	Sequence 193024,
30	13.8	69.0	18	11	US-10-310-914A-745552	Sequence 745552,
31	13.8	69.0	19	14	US-11-083-784-274670	Sequence 274670,
32	13.8	69.0	19	14	US-11-083-784-274670	Sequence 274670,
33	13.8	69.0	19	14	US-11-083-784-274670	Sequence 274670,
34	13.8	69.0	19	14	US-11-083-784-274670	Sequence 274670,
35	13.8	69.0	19	14	US-11-083-784-274670	Sequence 274670,
36	13.8	69.0	19	15	US-11-101-244-274031	Sequence 274031,
37	13.8	69.0	19	15	US-11-101-244-274065	Sequence 274065,
38	13.8	69.0	19	15	US-11-101-244-274126	Sequence 274126,
39	13.8	69.0	19	15	US-11-101-244-274153	Sequence 274153,
40	13.8	69.0	25	6	US-10-098-263B-58055	Sequence 58055, A
41	13.8	69.0	25	6	US-10-098-263B-58683	Sequence 58683, A
42	13.8	69.0	25	6	US-10-098-263B-58684	Sequence 58684, A
43	13.8	69.0	25	8	US-10-681-773-29903	Sequence 29903, A
44	13.8	69.0	25	8	US-10-681-773-40933	Sequence 40933, A
45	13.8	69.0	25	8	US-10-681-773-58064	Sequence 58064, A

ALIGNMENTS

RESULT 1

US-10-714-796-122

Sequence 122, Application US/10714796

Publication No. US20040180847A1

GENERAL INFORMATION:

APPLICANT: Dobie, Kenneth W.

TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION

FILE REFERENCE: ISHT-1004

CURRENT APPLICATION NUMBER: US/10/714,796

CURRENT FILING DATE: 2003-11-17

PRIOR APPLICATION NUMBER: US 10/156,603

PRIOR FILING DATE: 2002-05-23

NUMBER OF SEQ ID NOS: 237

SOFTWARE: PatentIn version 3.2

SEQ ID NO 122

LENGTH: 20

TYPE: DNA

ORGANISM: Homo sapiens

US-10-714-796-122

Query Match 100.0%; Score 20; DB 9; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATACAGCCA 20

Db 1 ACGTGAATTATACAGCCA 20

RESULT 2

US-10-476-597-63/c

Sequence 63, Application US/10476597

Publication No. US2004023576A1

GENERAL INFORMATION:

APPLICANT: Bullard, James

APPLICANT: Danjic, Nebojsa

APPLICANT: McHenry, Charles S.

TITLE OF INVENTION: System for Discovery of Agents that Block Yersinia Pestis and

TITLE OF INVENTION: Pseudomonas Aeruginosa DNA Replication

```
/ FILE REFERENCE: RDYN.02/PCT-US
/ CURRENT APPLICATION NUMBER: US/10/476,597
/ CURRENT FILING DATE: 2003-10-31
/ PRIOR APPLICATION NUMBER: US 60/290,725
/ PRIOR FILING DATE: 2001-05-14
/ PRIOR APPLICATION NUMBER: PCT/US02/15111
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: US 60/332,644
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 159
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 63
/ LENGTH: 40
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
US-10-476-597-63
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Query Match          76.0%; Score 15.2; DB 9; Length 40;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 ACGTGAATTATACCGACCA 20
         |||||
Db       27 ACGTGAATTACGACCGCA 8
```

```
RESULT 3
US-10-719-956-197295/C
/ Sequence 197295, Application US/10719956
/ Publication No. US20040146910A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Xue Mei Zhou
```

```
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
```

```
/ FILE REFERENCE: 3527.1
```

```
/ CURRENT APPLICATION NUMBER: US/10/719,956
```

```
/ CURRENT FILING DATE: 2003-11-20
```

```
/ PRIOR APPLICATION NUMBER: 60/427,836
```

```
/ PRIOR FILING DATE: 2002-11-20
```

```
/ NUMBER OF SEQ ID NOS: 699466
```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
/ SEQ ID NO 197295
```

```
/ LENGTH: 25
```

```
/ TYPE: DNA
```

```
/ ORGANISM: Rattus norvegicus
```

```
US-10-719-956-197295
```

```
Query Match          74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GTGGAATTATACCGCA 20
         |||||
Db       19 GTGGAATATACCTAGCA 2
```

```
RESULT 4
US-10-719-900-135431
```

```
/ Sequence 135431, Application US/10719900
```

```
/ Publication No. US20050026164A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Xue Mei Zhou
```

```
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
```

```
/ FILE REFERENCE: 3528.1
```

```
/ CURRENT APPLICATION NUMBER: US/10/719,900
```

```
/ CURRENT FILING DATE: 2003-11-20
```

```
/ PRIOR APPLICATION NUMBER: 60/427,808
```

```
/ PRIOR FILING DATE: 2002-11-20
```

```
/ NUMBER OF SEQ ID NOS: 982914
```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
/ SEQ ID NO 135431
```

```
/ LENGTH: 25
```

```
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-135431
```

```
Query Match          74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GTGGAATTATACCGCA 20
         |||||
Db       5 GAGGCATTATACCGCA 22
```

```
RESULT 5
US-10-719-900-265411/C
```

```
/ Sequence 265411, Application US/10719900
```

```
/ Publication No. US20050026164A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Xue Mei Zhou
```

```
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
```

```
/ FILE REFERENCE: 3528.1
```

```
/ CURRENT APPLICATION NUMBER: US/10/719,900
```

```
/ CURRENT FILING DATE: 2003-11-20
```

```
/ PRIOR APPLICATION NUMBER: 60/427,808
```

```
/ PRIOR FILING DATE: 2002-11-20
```

```
/ NUMBER OF SEQ ID NOS: 982914
```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
/ SEQ ID NO 265411
```

```
/ LENGTH: 25
```

```
/ TYPE: DNA
```

```
/ ORGANISM: Mus musculus
```

```
US-10-719-900-265411
```

```
Query Match          74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GTGGAATTATACCGCA 20
         |||||
Db       19 GTGGAATATACCTAGCA 2
```

```
RESULT 6
US-11-175-859-7489
```

```
/ Sequence 7489, Application US/11175859
```

```
/ Publication No. US20060024715A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Affymetrix, Inc.
```

```
/ TITLE OF INVENTION: Method of Analysis of Human Polymorphism
```

```
/ FILE REFERENCE: 3690.1
```

```
/ CURRENT APPLICATION NUMBER: US/11/175,859
```

```
/ CURRENT FILING DATE: 2005-07-05
```

```
/ PRIOR APPLICATION NUMBER: US 60/585,352
```

```
/ PRIOR FILING DATE: 2004-07-02
```

```
/ NUMBER OF SEQ ID NOS: 116251
```

```
/ SOFTWARE: PatentIn version 3.2
```

```
/ SEQ ID NO 7489
```

```
/ LENGTH: 50
```

```
/ TYPE: DNA
```

```
/ ORGANISM: homo sapien
```

```
US-11-175-859-7489
```

```
Query Match          74.0%; Score 14.8; DB 16; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 ACGTGAATTATACCGCA 20
         |||||
Db       8 ACATGTAATTAACAGCA 27
```

```
RESULT 7
```

```
US-11-175-859-91821/c
; Sequence 91821, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91821
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-91821

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 16; Length 50;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGTGATTATACCAAGCC 19
Db 48 CATGGAATTATACCAAGCC 31

RESULT 8
US-10-719-900-962131/c
; Sequence 962131, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 962131
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-962131

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 9; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGAATTATACCAAGCC 20
Db 20 GGAATGATACCAAGCC 5

RESULT 9
US-10-719-956-169821
; Sequence 169821, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169821
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-169821

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGTGATTATACCAAGCC 19
Db 6 ACGTGAGTGATACCAAGCC 24

RESULT 10
US-10-719-956-169822
; Sequence 169822, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169822
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-169822

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGTGATTATACCAAGCC 19
Db 6 ACGTGAGTGATACCAAGCC 24

RESULT 11
US-10-719-900-467341
; Sequence 467341, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 467341
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-467341

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 9; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGTGATTATACCAAGCC 19
Db 5 ACGTGAGTGATACCAAGCC 23

RESULT 12
```

```
US-10-956-157-15043/c
; Sequence 15043, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15043
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-15043

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CGTGAATTATACAGCCA 20
        ||||| ||||| |||||
Db      19 CGTGAAGATATACAGCCA 1

RESULT 13
US-10-956-157-15044/c
; Sequence 15044, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15044
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-15044

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CGTGAATTATACAGCCA 20
        ||||| ||||| |||||
Db      20 CGTGAAGATATACAGCCA 2

RESULT 14
US-10-956-157-190558/c
; Sequence 190558, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 190558
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-190558

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CGTGAATTATACAGCCA 20
        ||||| ||||| |||||
Db      20 CGTGAAGATATACAGCCA 2

RESULT 15
US-10-932-182A-135456
; Sequence 135456, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 135456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-135456

Query Match          71.0%; Score 14.2; DB 11; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 ACGTGAATTATACAGCC 19
        ||||| ||||| |||||
Db      5 ACGTCCGATTATACAGCC 23
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Search completed: May 23, 2006, 11:53:35
Job time : 979 secs

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OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 11:37:18 ; Search time 50 Seconds
(without alignments)
28.222 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgtggaattatcacgcga 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 393418

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

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3: /EMC_Celestra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB_seq.*
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6: /EMC_Celestra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB_seq.*
7: /EMC_Celestra_SIDS3/ptodata/2/pubpna/US12_NEW_PUB_seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	25	US-11-217-529-135456	Sequence 135456, A
2	13.8	69.0	25	US-11-217-529-115814	Sequence 115814, A
3	13.6	68.0	25	US-11-238-282-11	Sequence 11, Appl
4	13.4	67.0	25	US-11-217-529-184614	Sequence 184614, A
5	13.2	66.0	25	US-11-217-529-55862	Sequence 55862, A
6	12.8	64.0	25	US-11-217-529-45848	Sequence 45848, A
7	12.8	64.0	25	US-11-217-529-61089	Sequence 61089, A
8	12.8	64.0	25	US-11-217-529-92822	Sequence 92822, A
9	12.8	64.0	25	US-11-217-529-103876	Sequence 103876, A
10	12.6	63.0	25	US-11-217-529-6691	Sequence 6691, Ap
11	12.6	63.0	25	US-11-217-529-23381	Sequence 23381, A
12	12.4	62.0	25	US-11-217-529-112299	Sequence 112299, A
13	12.4	61.0	25	US-11-217-529-8938	Sequence 8938, Ap
14	12.2	61.0	25	US-11-217-529-13433	Sequence 13433, A
15	12.2	61.0	25	US-11-217-529-36205	Sequence 36205, A
16	12.2	61.0	25	US-11-217-529-36523	Sequence 36523, A
17	12.2	61.0	25	US-11-217-529-179966	Sequence 179966, A
18	12.2	61.0	25	US-11-217-529-189355	Sequence 189355, A
19	12.2	61.0	25	US-11-217-529-193006	Sequence 193006, A
20	12.2	61.0	25	US-11-217-529-193007	Sequence 193007, A
21	12.2	61.0	25	US-11-217-529-193009	Sequence 193009, A
22	12.2	61.0	25	US-11-217-529-11032	Sequence 11032, A
23	12.2	60.0	25	US-11-217-529-33385	Sequence 33385, A
24	12.2	60.0	25	US-11-217-529-33692	Sequence 33692, A
25	12.2	60.0	25	US-11-217-529-61237	Sequence 61237, A

c	26	12	60.0	25	7	US-11-217-529-93539	Sequence 93539, A
c	27	12	60.0	25	7	US-11-217-529-105215	Sequence 105215, A
c	28	12	60.0	25	7	US-11-217-529-146223	Sequence 146223, A
c	29	12	60.0	25	7	US-11-217-529-169263	Sequence 169263, A
c	30	12	60.0	51	7	US-11-143-642-1422	Sequence 1422, Ap
c	31	11.8	59.0	25	7	US-11-217-529-37938	Sequence 37938, A
c	32	11.8	59.0	25	7	US-11-217-529-92308	Sequence 92308, A
c	33	11.8	59.0	25	7	US-11-217-529-107278	Sequence 107278, A
c	34	11.8	59.0	25	7	US-11-217-529-114640	Sequence 114640, A
c	35	11.8	59.0	25	7	US-11-217-529-122996	Sequence 122996, A
c	36	11.8	59.0	25	7	US-11-217-529-129513	Sequence 129513, A
c	37	11.8	59.0	25	7	US-11-217-529-193004	Sequence 193004, A
c	38	11.8	59.0	25	7	US-11-217-529-193011	Sequence 193011, A
c	39	11.6	58.0	25	7	US-11-217-529-28242	Sequence 28242, A
c	40	11.6	58.0	25	7	US-11-217-529-33205	Sequence 33205, A
c	41	11.6	58.0	25	7	US-11-217-529-34626	Sequence 34626, A
c	42	11.6	58.0	25	7	US-11-217-529-54791	Sequence 54791, A
c	43	11.6	58.0	25	7	US-11-217-529-61646	Sequence 61646, A
c	44	11.6	58.0	25	7	US-11-217-529-72067	Sequence 72067, A
c	45	11.6	58.0	25	7	US-11-217-529-72753	Sequence 72753, A

ALIGNMENTS

RESULT 1
US-11-217-529-135456
Sequence 135456, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORO LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 135456
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-135456
Query Match 71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 5 ACGTCCATTATTCACGCC 23
US-11-217-529-115814
Sequence 115814, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORO LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115814
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-115814

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGAG 17
DB 5 ACGTGAATTATACGAG 21

RESULT 3
US-11-238-282-11
; Sequence 11, Application US/11238282
; Publication No. US20060089303A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Cancer-Testis Antigens
; FILE REFERENCE: I0461.70125US01
; CURRENT APPLICATION NUMBER: US/11/238,282
; CURRENT FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: US 10/054,683
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/280,718
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/285,154
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/327,432
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-11-238-282-11

Query Match 68.0%; Score 13.6; DB 7; Length 29;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGAGCA 20
DB 3 ACGTGAATTATACGAGCA 22

RESULT 4
US-11-217-529-184614/c
; Sequence 184614, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 184614
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-184614

Query Match 67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGATTATACGAGC 18
DB 22 TGGATTATACGAGC 8

RESULT 5
US-11-217-529-55862/c
; Sequence 55862, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-55862

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTGAATTATACGAGCC 19
DB 19 CTTGAGTTATACCTGCC 2

RESULT 6
US-11-217-529-45848
; Sequence 45848, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3

SEQ ID NO 45848
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-45848

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAATTATACCGCCA 20
|||||
DB 1 GGAATTATACCGCCA 16

RESULT 7
US-11-217-529-61089
; Sequence 61089, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61089
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-61089

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAATTATACCGCCA 20
|||||
DB 1 GGAATTATACCGCCA 16

RESULT 8
US-11-217-529-92822/C
; Sequence 92822, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 92822
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-92822

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAATTATACCGCCA 20
|||||
DB 19 GCAATGATATACCGCCA 4

RESULT 9
US-11-217-529-103876
; Sequence 103876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 103876
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-103876

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTGGAATTATACCG 17
|||
DB 8 CGCAGAAATTATACCG 23

RESULT 10
US-11-217-529-6691
; Sequence 6691, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-6691

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      1  ACGTGAATTATACCAGCC  19
          ||| | | | | | | |
Db      6  ACATGCATTATTCACGCC  24

```

```

RESULT 11
US-11-217-529-23381
Sequence 23381, Application US/11217529
Publication No. US2006009612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23381
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-23381

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Query Match	63.0%	Score 12.6;	DB 7;	Length 25;
Best Local Similarity	78.9%	Pred. No. 81;		
Matches 15; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

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QY      1  ACGTGAATTATACCAGCC 19
         |||||  |||||
Db      2  ACGTGAACAGTACCAGCC 20

```

```

RESULT 12
US-11-217-529-112299/c
Sequence 112299, Application US/11217529
Publication No. US2006009612A1
GENERAL INFORMATION:
APPLICANT: SUNTOY LIMITED
APPLICANT: NAKAO, YOSHIRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIHO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, YOSHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: 182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 112299
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-112299

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Query Match	62.0%;	Score 12.4;	DB 7;	Length 25;
Best Local Similarity	92.9%;	Pred. No. 1e+02;		
Matches 13; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	ACGTGAATTATAC	14
LF	15	ACGTGATAATAC	2

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RESULT 13
US-11-217-529-8938
? Sequence 8938, Application US/11217529
? Publication No. US20060099612A1
? GENERAL INFORMATION:
? APPLICANT: SUNTORY LIMITED
? APPLICANT: NAKAO, YOSHIHIRO
? APPLICANT: NAKAMURA, NORIHISA
? APPLICANT: KODAMA, YUKIKO
? APPLICANT: FUJIMURA, TOMOKO
? APPLICANT: ASHIKARI, TOSHIHIKO
? TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
? FILE REFERENCE: S-38-285
? CURRENT APPLICATION NUMBER: US/11/217,529
? CURRENT FILING DATE: 2005-09-02
? PRIOR APPLICATION NUMBER: US 10/932,182
? PRIOR FILING DATE: 2004-09-02
? NUMBER OF SEQ ID NOS: 197023
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 8938
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Saccharomyces pastorianus
US-11-217-529-8938

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Query Match	61.0%	Score 12.2	DB 7	Length 25
Best Local Similarity	82.4%	Pred. No. 1.3e+02		
Matches 14; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 3 GTGGAATTATACCAGCC 19
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Db 4 GTGGACATATACCACCC 20

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RESULT 14
US-11-217-529-13433/c
? Sequence 13433, Application US/11217529
? Publication No. US2006099612A1
? GENERAL INFORMATION:
? APPLICANT: SUNTORY LIMITED
? APPLICANT: NAKAO, YOSHIHIRO
? APPLICANT: NAKAMURA, NORIHISA
? APPLICANT: KODAMA, YUKIKO
? APPLICANT: FUJIMURA, TOMOKO
? APPLICANT: ASHIKARI, TOSHIKO
? TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
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? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 13433
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Saccharomyces pastorianus
US-11-217-529-13433

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Query Match	61.0%;	Score 12.2;	DB 7;	Length 25;
Best Local Similarity	82.4%;	Pred. No. 1.3e+02;		
Matches 14; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

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; US-11-217-529-36205/c
; ; Sequence 36205, Application US/11217529
; ; Publication No. US20060099612A1
; ; GENERAL INFORMATION:

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APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 36205
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-36205

Query Match 61.0%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 24 ACGTGAAGCATCCGAG 8

Search completed: May 23, 2006, 11:54:31
Job time : 50 secs

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